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Conference Abstract

Getting the GIST: Testing an integrative data structure for linking taxonomy, biodiversity and conservation

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Abstract

Assessing and addressing biodiversity needs are of critical and time-sensitive importance, with the post-2020 Global Biodiversity Framework's Global Taxonomy Initiative underscoring the need to build capacity in how we conceptualize biodiversity (Abrahamse et al. 2021). Species—as biological units—and their names are the backbone for the data integration and synthesis needed for biodiversity research and conservation decision-making (Grace et al. 2021). In integrating name sources for a single taxonomic group, barriers frequently limit linking species names across regional and global authoritative

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sources. In response to such challenges, **we present a case study testing a Globally Integrated Structure of Taxonomy (GIST) to ensure the integration of taxonomy in biodiversity and conservation sciences**. This framework characterizes the components enabling transparent association of species names through synonymy (alternate names or spellings), authorship, specimens, versions and timestamps, and taxonomic relationships in space and time.

Taxonomy provides a critical link between biodiversity data types and databases. Efforts towards global taxonomic integration are confounded by insufficient connectivity between taxonomic assemblages, with implications for research, monitoring, and conservation practice (Christie et al. 2021, Jetz et al. 2019, McClure et al. 2020). In attempting to match multiple taxonomic groups across databases, **we highlight current progress and remaining challenges to produce and use a GIST**. We evaluate the standardized, comprehensive taxonomies of mammals, birds, reptiles, amphibians, dragonflies and damselflies, butterflies, ants, plants, and crabs produced for the Map of Life project (Jetz et al. 2012), identifying which missing components impede their utility. We show that for terrestrial mammals, GIST standards are almost fulfilled, but for invertebrate taxa, such as butterflies, GIST standards are unmet, resulting in broken taxonomic links between aggregators of genetic, spatial, functional, and physical data. We find that even the comprehensive taxonomies we examine do not harmonize well with taxonomies of global genetics, phylogenetics, macroecology, and conservation databases. This is because current taxonomic data infrastructures on biodiversity respositories lack the necessary structural components, searchability, and name source transparency to fully integrate taxonomies, as different independently advancing data sources lack standard metadata practices and operable interfaces. The GIST components enable data linkage and provide clear sourcing and metadata, enabling taxonomic data accessibility, reuse, and interoperability. This structure can act as a step toward open and FAIR (Findable, Accessible, Interoperable, and Reusable) data practice as it relates to taxon names (Wilkinson et al. 2016). Without transparent, integrated, accessible, and updated taxonomic information, macroecological inferences and conservation decisions for even charismatic groups are impeded.

Keywords

taxonomic backbone, integrative science, data linkage, social infrastructure

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